Multimodal MRI Brain Glioma Segmentation Combining Grayscale Histogram and Cellular Automata Postprint

Authors: Yi Fei, Gong Jing, Duan Huihong, Su Guanqun, Tian Hailong, Nie Shengdong

Date: 2018-06-19T00:00:00+00:00

Abstract

To address the problem of inaccurate segmentation caused by blurred and complex boundaries of brain gliomas, a brain glioma segmentation algorithm combining gray level histogram (GLH) with improved cellular automata is proposed. First, T2-weighted images and fluid-attenuated inversion recovery (FLAIR) images of brain gliomas are fused; then, the glioma region is enhanced by utilizing the characteristics of the gray level histogram; finally, segmentation is performed using improved cellular automata with weighted distance as the feature vector, and segmentation results for various glioma tissues are obtained. Segmentation experiments were conducted on 20 datasets from the BraTS2015 (brain tumor segmentation) database and 10 clinical glioma datasets, achieving average segmentation accuracies of 90.76% and 89.73% for the whole tumor region and tumor core region, respectively. Experimental results demonstrate that, compared with comparative methods, the proposed algorithm not only better segments glioma regions with conspicuous contrast, but also partially solves the problem of inaccurate segmentation of blurred glioma regions. Moreover, the algorithm improves segmentation accuracy and robustness without increasing algorithmic complexity.

Full Text

Preamble

Brain Glioma Segmentation for Multi-modality MR Images Based on Gray Level Histogram and Cellular Automata

Yi Fei[1], Gong Jing[1], Duan Huihong[1], Su Guanqun[1], Tian Hailong[2], Nie Shengdong[1]
(1. Institute of Medical Imaging Engineering, University of Shanghai for Science

& Technology, Shanghai 200093, China;
2. Neurosurgery Department, Qilu Hospital of Shandong University, Qingdao, Shandong 266035, China)

Abstract: The fuzzy and complex boundaries of brain gliomas often lead to inaccurate segmentation. To address this problem, this paper proposes a novel glioma segmentation algorithm that combines gray level histogram (GLH) with an improved cellular automaton. First, the T2-weighted and fluid attenuated inversion recovery (FLAIR) MR images of brain glioma are fused. Then, histogram features are utilized to enhance the glioma region. Finally, the improved cellular automaton performs segmentation using weighted distance as the feature vector to obtain the segmentation results of various glioma tissues. Experiments were conducted on 20 groups of data from the BraTS2015 (Brain Tumor Segmentation) database and 10 groups of clinical glioma data. The average segmentation accuracy for the entire tumor region and core tumor region reached 90.76% and 89.73%, respectively. Experimental results demonstrate that compared with contrast methods, the proposed algorithm not only better segments glioma regions with obvious contrast but also alleviates the problem of inaccurate segmentation in fuzzy glioma regions to some extent. Moreover, the algorithm improves segmentation accuracy and robustness without increasing computational complexity.

Keywords: brain glioma; multi-modality magnetic resonance image; image segmentation; image fusion; gray level histogram; cellular automata

0 Introduction

Brain glioma segmentation is a crucial yet challenging task in surgical planning and treatment, forming the foundation for subsequent glioma assessment. In clinical practice, glioma is the most common primary brain tumor in adults, originating from glial cell mutations and infiltrating surrounding tissues. Gliomas account for 81% of malignant brain tumors, with high morbidity and mortality rates. Glioblastoma patients have particularly low overall survival rates, with 5-year survival rates as low as 0.05%~4.7% and average survival not exceeding 14 months. Clinicians typically perform manual segmentation of tumor images layer by layer based on clinical experience, which is not only time-consuming but also yields subjective results with low reproducibility. Therefore, accurate and effective automatic or semi-automatic segmentation of brain glioma is essential.

The boundaries of brain gliomas are blurred and their internal structures are complex. Single-modality MRI cannot provide sufficient image information. As shown in [Figure 1: see original paper], T1C images highlight the core tumor region (marked by yellow arrows), including enhanced and necrotic parts, while T2 and FLAIR images show edema regions as hyperintense areas (marked by green arrows). Consequently, this paper utilizes three modalities of MR brain glioma images—T1C, T2, and FLAIR—for glioma segmentation.

1 Research Methods

1.1 Algorithm Flow

The algorithm framework is illustrated in [Figure 2: see original paper]. T1C images are used to segment the core region of brain glioma, while the fused T2 and FLAIR images segment the edema region. The algorithm consists of three main steps: (a) fusing FLAIR and T2 modalities of brain glioma images; (b) performing gray level histogram transformation; and (c) segmenting brain glioma using the improved cellular automata algorithm to obtain complete segmentation results.

Cellular automata (CA) are widely applied in image denoising, enhancement, segmentation, and security. Compared with other segmentation methods, CA is simple to implement and highly flexible. In recent years, researchers have proposed various tumor segmentation methods using CA. For instance, Desbordes et al. considered spatial information by introducing a 26-Moore neighborhood system and adding neighborhood similarity information to the CA transition function. Sompong et al. proposed an FCM-CA model that extracts tumor image features using gray-level co-occurrence matrices, classifies these features into four categories using FCM, and then improves the CA transition function using the two feature categories representing tumor regions. Hamamci et al. proposed a CA-Level Set model that utilizes the Grow Cut transition function with adaptive parameters to adjust the transition function to an optimal state. However, due to the complexity of brain glioma images and significant variations between cases, parameter optimization becomes difficult, leading to overly rapid decay of the transition function. Sompong et al. introduced the concept of neighborhood-weighted distance, converting image grayscale information into weighted distance information, which effectively solved the problem of rapid transition function decay. However, this method lacks neighborhood similarity information and requires improvement.

Most brain glioma tissues are blurred, making segmentation difficult. To address this issue, Sachdeva et al. proposed an active contour model combining image texture information, which utilizes tumor texture and brightness information to establish static and dynamic fields, enabling the initial contour to evolve accurately to tumor boundaries. However, this method does not segment complete tumor tissues. Randhawa et al. used cross-entropy loss functions for accurate classification of tumor edge pixels. Their algorithm first performs preliminary classification of brain glioma images using DNN, then assigns larger weights to edge pixels in the cross-entropy loss function and adds rules to prevent over-segmentation. However, the computational load is substantial, and local optima problems occur with insufficient data.

These methods primarily address specific problems in brain glioma segmentation, with few accurately segmenting edema regions. To further improve edema region segmentation accuracy and solve under-segmentation caused by rapid transition function decay, this paper proposes a multi-modality MRI brain

glioma segmentation algorithm combining gray level histogram characteristics with improved cellular automata. Experimental results on BraTS2015 data and clinical data demonstrate that the algorithm exhibits good robustness and can accurately segment complete brain gliomas.

1.2 Image Fusion

Segmenting brain glioma edema using single-modality images presents many defects. As shown in the first row of Figure 3: see original paper, for cases where the glioma region connects to the ventricle, using only T2-modality brain glioma images causes over-segmentation. Conversely, using only FLAIR-modality images may result in incomplete segmentation, as shown in the second row of Figure 3: see original paper, which does not display the entire glioma region. Therefore, fusing T2 and FLAIR modalities effectively displays the complete brain glioma region while reducing interference from redundant information around single-modality gliomas.

Wavelet transform-based image fusion is a current research focus. Wavelet transform extracts low-frequency information while obtaining high-frequency information in horizontal, vertical, and diagonal directions, facilitating higher-level processing of decomposed information and improving fusion effects. The fusion objective is to completely display the glioma region while maintaining clear edge information. Literature indicates that combining edge operators can better preserve image details and ensure clarity.

This paper employs the Daubechies wavelet model. According to Mallat' s algorithm, two images to be fused are decomposed to obtain low-frequency components, where j represents the decomposition level, and $h,\ v,\ d$ represent horizontal, vertical, and diagonal directions, respectively.

The local variance fusion rule is used to fuse corresponding components from both images. The local variance calculation method is shown in Equation (1), where $m,\ n$ represent the local matrix size (m=n=3), and μ denotes the matrix mean value.

When the local variance is too small, image distortion occurs in the fused result. Therefore, the Canny operator is used to extract edges from high-frequency components, followed by local variance calculation on high-frequency edge components.

The low-frequency component fusion criterion for images A and B is shown in Equation (2), where represents the fused low-frequency coefficient.

High-frequency component fusion criteria are shown in Equations (3)-(5), where and represent the high-frequency coefficients of images A and B after Canny edge detection, and represent the local variance of high-frequency edge components, and is the fused high-frequency coefficient containing three directions.

Finally, wavelet inverse transform is performed on the obtained fusion coeffi-

cients to produce the fused image. As shown in Figure 3: see original paper, the wavelet fusion model effectively fuses T2 and FLAIR modalities of brain glioma images.

1.3 Gray Level Histogram Characteristics

T1C images can effectively display enhanced and necrotic parts of brain glioma, but low-grade gliomas lack obvious enhancement or necrosis regions, making core tumor regions blurred in T1C images. The gray level difference between edema boundaries in fused images and blurred tumor regions in T1C images with normal tissue is small, easily leading to inaccurate segmentation. Gray level histograms reflect image gray distribution and dynamic range, enabling region of interest segmentation and enhancement. Therefore, this paper utilizes gray level histogram characteristics of brain glioma images to enhance glioma regions in fused and T1C images while suppressing normal regions.

[Figure 4: see original paper] illustrates the GLH (gray level histogram) processing procedure using fused brain glioma images as input, which also applies to T1C images. Brain glioma regions differ in gray level from normal tissue regions, and tumors occupy less brain volume than normal tissue. As shown in Figure 4: see original paper(e), normal brain region gray values concentrate at histogram peak-valley positions, indicating larger normal tissue volume, while tumor and boundary region gray values concentrate at descending and tail regions. Figure 4: see original paper(f) intuitively reflects these characteristics, where tumor region gray value frequencies are lower than normal tissue frequencies. Using this feature, Equation (6) reconstructs values at each pixel, where is the gray value and represents its occurrence probability. c denotes the maximum gray value representable by image bit depth, and is the weight coefficient. Experimental validation shows optimal image conversion when ranges from 0.006 to 0.009.

After processing, Figure 4: see original paper is obtained. The tumor portion is prominently displayed with clearer boundaries. To more intuitively demonstrate this conclusion, a 5×5 matrix centered at boundary pixel points (in red) is extracted. As shown in Figure 4: see original paper(h), the gray difference between boundary and background regions increases after transformation, while normal tissue gray values are effectively suppressed. Compared with the original image, the boundary between brain glioma and normal tissue becomes clearer, facilitating subsequent segmentation.

1.4 Improved Cellular Automata Algorithm

CA is a pixel-based algorithm that treats each image pixel as a cell evolving and classifying according to a transition function within a specific limited neighborhood system, influenced by neighboring cells, and enabling multi-class image segmentation. CA adopts a Moore-type eight-neighborhood system. As shown in Equation (7), q is a neighboring pixel of p.

The transition function is shown in Equation (8), where and represent 3×3

neighborhoods centered at p and , respectively, and represent coordinates of p and , and represent the mean square error of the distance neighborhoods.

The above transition function only considers grayscale relationships between two pixels, which cannot accurately determine edge positions. As shown in [Figure 5: see original paper], the central point 10 has equal grayscale differences with pixels in its 3×3 neighborhood, making accurate region classification impossible. However, neighboring pixels belong to different regions. In [Figure 5: see original paper], the two eight-neighborhoods centered at 12 and 8 differ and have different similarity levels with the eight-neighborhood centered at 10. Based on these features, this paper transforms pixel relationships into neighborhood relationships, effectively distinguishing pixels with similar gray levels.

The weight coefficient for neighborhood point is described in Equation (11), where adjusts weights to appropriate positions (=0.1 in this paper), as shown in Figure 7: see original paper.

Using grayscale values alone as feature vectors for evolution classification causes exponential transition function decay. To reduce this decay and accurately locate boundaries, this paper converts grayscale relationships between pixels into weighted distance relationships. Figure 6: see original paper(c) show evolution results using grayscale and mean square error weighted distance as feature vectors, respectively, with =0.05. In Figure 6: see original paper, the transition function experiences excessive decay even in the same region, causing indistinguishable boundaries and final decay results of 0.0005. Figure 6: see original paper solves the rapid decay problem and effectively distinguishes boundaries from flat regions.

The transformation results show that weighted distances are smaller for pixels in the same region as seed points and larger otherwise, consistent with the principle that gray values are similar within the same region and differ significantly between regions. However, since weighted distance values between pixels are smaller than grayscale differences, transition function decay can be effectively reduced. Therefore, the transition function is defined as.

The mean square error weighted distance cellular automata algorithm flow is shown in .

2 Experimental Results and Analysis

2.1 Algorithm Accuracy Analysis

To validate the proposed algorithm' s effectiveness, segmentation experiments were conducted on 20 groups of clinical data from the BraTS2015 database (including 10 High-Grade Glioma (HGG) and 10 Low-Grade Glioma (LGG) cases) and 10 groups of actual clinical glioma data from Qilu Hospital of Shandong University (7 HGG and 3 LGG cases). The HGG segmentation results in the database include edema, enhancement, and necrosis parts. Since LGG enhancement and necrosis parts are difficult to distinguish, segmentation results include

edema and core (enhancement+necrosis) parts. The actual clinical data lacks strict gold standards distinguishing enhancement and necrosis, so only core and edema parts were segmented.

All BraTS2015 database images had skulls removed, were strictly aligned with T1 images, and isotropically interpolated to 1mm resolution. Images were acquired at 3T field strength, sized 240×240 pixels, and included gold standards. The clinical brain glioma data from Qilu Hospital included gold standards manually segmented by senior radiology experts, with 6mm slice thickness, 1.5T field strength, and 336×336 pixel size.

In experiments, 10 layers containing brain glioma were randomly selected from each case in the BraTS2015 database for segmentation. The final quantitative evaluation for each case represents the average of 10 segmentation results. Due to thicker slices in the Qilu Hospital data, 5 layers were selected.

The experimental environment used an Intel i5 processor at 3.2 GHz with 8 GB RAM. Dice Similarity Coefficient (DSC), False Positive Rate (FPR), and Sensitivity (Sens.) served as quantitative evaluation metrics. True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) are defined as follows: , where T is the sum of pixels in the actual glioma location and R is the sum of pixels in the segmentation result. DSC is defined as: . FPR is defined as: . Sensitivity is defined as: .

For Equation (6), was varied from 0.001 to 0.012 in steps of 0.003 to obtain DSC and FPR values for whole tumor segmentation, as shown in Figure 8: see original paper. When ranges from 0.006 to 0.012, DSC reaches its maximum and stabilizes. However, when is between 0.009 and 0.012, FPR increases, raising the probability of tumor mis-segmentation. Therefore, values between 0.006 and 0.009 yield optimal segmentation results. For Equation (11), and in Equation (13) were varied from 0.01 to 0.25 in steps of 0.05, starting from 0.005, to calculate DSC metrics for whole tumor segmentation. Figure 8: see original paper shows that achieves optimal value at 0.1, while has minimal impact on results, demonstrating the robustness of using weighted distance as the feature vector.

[Figure 9: see original paper] shows segmentation results for two HGG cases, segmenting the whole tumor on GLH-transformed fused images and the core tumor on original TIC images. HGG core regions are relatively distinct while edema regions are blurred. GLH transformation on fused images highlights glioma regions and effectively suppresses normal tissue. [Figure 10: see original paper] shows results for two LGG cases. For LGG, both core and edema regions lack obvious imaging features, making tumor boundaries indistinguishable. Therefore, gray level histogram characteristic transformation was applied to both fused and T1C images, as shown in Figure 10: see original paper(b). Whole and core LGG regions were then segmented from Figure 10: see original paper(b), with results shown in Figure 10: see original paper(d). [Figure 11: see original paper] first row overlays whole and core tumor segmentation results

according to spatial relationships. In the first two columns, pink represents edema, green represents enhancement, and blue represents necrosis. In the last two columns, pink represents edema and green represents core region. The second row shows gold standards, demonstrating high similarity with segmentation results.

For further validation, quantitative evaluation was performed on whole and core tumor segmentation results for all 30 data groups, with comparative analysis against the CA-Level set model and Grow Cut model. Grow Cut is a classic CA algorithm, while CA-Level set combines improved cellular automata with level set methods.

[Figure 12: see original paper] shows that the proposed algorithm achieves superior segmentation results. For HGG and LGG cases in the database, average DSC values for whole tumor segmentation are 0.93 and 0.92, respectively. Average DSC values for HGG core tumor and enhancement parts reach 0.95 and 0.90, respectively, while LGG core tumor segmentation achieves 0.89. Since HGG shows more distinct enhancement and necrosis while LGG features are less obvious with blurred tissue structures, HGG segmentation results are relatively better. For actual clinical glioma data without skull removal and with more complex cases, some gliomas grow at skull edges, yielding slightly lower results than database cases. Average DSC values for whole and core tumor regions are 0.88 and 0.86, respectively.

provides quantitative comparison with CA-Level set and Grow Cut models. The proposed algorithm significantly outperforms both methods. For HGG in the database, with more distinct tissue differences, both whole and core part segmentation results are good. The proposed algorithm achieves average DSC and Sens. values of 0.937 and 0.916, respectively, with smaller inter-case variation and lower false positive rates than other methods. Since core tumor boundaries are clearer, contrast methods show smaller DSC values for whole tumor segmentation than for core tumor. For LGG and clinical glioma, where edema and core boundaries are blurred and clinical cases are complex with lower image quality, the proposed algorithm' s average DSC and Sens. values are slightly lower than for HGG in the database, with slightly higher FPR values. However, results remain significantly superior to contrast methods.

For LGG, average DSC and Sens. values reach 0.902 and 0.89, respectively. For clinical glioma, average DSC and Sens. values are 0.869 and 0.852, respectively. Contrast methods also show lower values for LGG and ClG whole and core tumor segmentation than for HGG, with the lowest values for ClG.

The CA-Level set model can adjust the transition function to achieve good segmentation states and optimizes results using level set algorithms, performing better than Grow Cut. Grow Cut suffers from premature evolution termination, causing under-segmentation. The CA-Level set model uses level sets to smooth edges, requiring high initial contour quality and difficult parameter optimization, leading to inaccurate edge localization. These problems directly cause lower

DSC and Sens. values.

As shown in [Figure 13: see original paper], the proposed algorithm's DSC values exceed those of both contrast algorithms, with lower and more stable FPR values in some cases. Due to complex HGG structures often connecting to ventricles, contrast methods yield higher FPR values. For LGG and clinical glioma with low contrast and diverse, complex manifestations, contrast methods tend to produce under-segmentation. The proposed algorithm addresses these issues in CA-Level set and Grow Cut models, achieving better results. Experimental results demonstrate that the proposed algorithm can accurately segment brain gliomas with high robustness.

The algorithm' s robustness manifests in parameter variation resistance and case diversity resistance. is the core parameter controlling transition function evolution trends and affecting segmentation results. Figure 14: see original paper records DSC values as varies from 0.1 to 0.7. The proposed algorithm maintains high overlap rates while remaining largely unaffected by , showing stable performance. Contrast methods vary significantly with changes, with optimal segmentation around =0.5.

Variance of DSC values across algorithms for three case types reflects result disparities—larger values indicate greater gaps and poorer robustness. Figure 14: see original paper shows that the proposed algorithm' s variance is smaller than contrast methods vertically, indicating better robustness within single case types. Horizontally, the proposed algorithm's variance across different case types is smaller, demonstrating better robustness to case diversity. Contrast methods show larger disparities across case types, especially for LGG, indicating poor robustness for low-grade glioma segmentation.

2.2.1 Operation Complexity Analysis

The proposed algorithm consists of three main parts, with computational complexity concentrated in these steps. Image fusion incurs complexity in matrix fusion as shown in Equations (2) and (5), with other lines having constant complexity. Image gray level histogram conversion has complexity. The improved CA algorithm' s computational complexity for calculating mean square error weighted distance and initializing seed templates is , while CA evolution complexity is . Thus, overall complexity is . Grow Cut, derived from CA, lacks image preprocessing but has pixel evolution classification complexity of . The CA-Level set model' s CA portion has complexity , and level set evolution also has , making total complexity . While complexity is similar across three algorithms, operation time differs as shown in . Classic Grow Cut processes entire images, wasting time on non-ROI regions. The proposed algorithm and CA-Level set algorithm process only ROI regions, significantly reducing runtime. The proposed algorithm' s runtime mainly concentrates on the improved CA segmentation step, as converting grayscale to weighted distance information consumes time relative to original CA. The CA-Level set algorithm' s level

set portion also requires time until convergence, with average operation time slightly shorter than the proposed algorithm.

Experiments show that both the proposed algorithm and CA-Level set algorithm' s runtime relates to ROI region size. Five values between maximum and minimum ROI sizes were compared, as shown in Figure 15: see original paper. Both algorithms' runtime increases with ROI size. Since the proposed algorithm' s computation concentrates on pixel classification, its runtime is more affected by ROI size—shorter for small ROIs and increasing faster for larger inputs. The CA-Level set algorithm' s level set portion is less related to ROI size, primarily connected to the CA portion, increasing with ROI but more slowly than the proposed algorithm.

2.2.2 Space Complexity Analysis

All three methods have comparable space complexity, as shown in last column. The proposed algorithm releases space promptly during operation without storing intermediate results, reducing storage requirements and demanding slightly less memory than CA-Level set on average. Grow Cut is relatively simple with low space complexity and minimal memory demand. Memory consumption versus ROI region size was compared in Figure 15: see original paper. Memory demand increases with ROI size but stabilizes beyond certain values. Overall, all three algorithms have modest memory requirements.

3 Conclusion

This paper proposes a multi-modality MRI brain glioma segmentation algorithm combining gray level histogram with cellular automata. First, fusing T2 and FLAIR modalities of brain glioma images can supplement edema region display while suppressing surrounding redundant information. Second, using gray level histogram characteristics of brain glioma images highlights tumor regions, alleviating inaccurate segmentation caused by blurred tumor regions. Third, converting image grayscale information to weighted distance information slows transition function decay, enabling effective distinction between boundaries and flat regions. Moreover, fully utilizing pixel spatial information better distinguishes similar regions. Experimental results demonstrate that the proposed algorithm can accurately segment brain gliomas with high stability.

Brain glioma segmentation is fundamental for radiotherapy, surgical planning, and benign/malignant assessment. Clinically, doctors primarily rely on surgical navigation, fluorescent staining, and other auxiliary technologies to determine glioma locations. However, existing technologies are immature. For some low-grade or complex gliomas where imaging features differ minimally between glioma and normal tissue, accurate glioma contour delineation is impossible, failing to meet clinical needs. This urgent problem requires solution. This paper uses gray level histogram characteristics to highlight blurred tumor regions and suppress surrounding redundant tissue, partially solving this problem. Although

two-modality image fusion can reduce redundant information around gliomas, some interference remains at brain glioma edges after gray level histogram transformation, affecting segmentation accuracy. Future research should focus on reducing this interference while maximizing blurred glioma region highlighting. Automation degree is also clinically important—higher automation reduces human intervention, avoids doctor subjectivity, and reduces misdiagnosis rates. Therefore, future research should combine clinical applications to meet clinical demands.

References

[1] Menze B H, Jakab A, Bauer S, et al. The multimodal brain tumor image segmentation benchmark (BRATS) [J]. IEEE Trans on Medical Imaging, 2015, 34 (10): 1993-2024.

[2] Ostrom Q T, Bauchet L, Davis F G, et al. The epidemiology of glioma in adults: a "state of the science" review [J]. Neuro-oncology, 2014, 16 (7): 896-913.

[3] Van Meir E G, Hadjipanayis C G, Norden A D, et al. Exciting new advances in neuro-oncology: The avenue to a cure for malignant glioma [J]. CA: A Cancer Journal for Clinicians, 2010, 60 (3): 166-193.

[4] Sompong C, Wongthanavasu S. An efficient brain tumor segmentation based on cellular automata and improved tumor-cut algorithm [J]. Expert Systems with Applications, 2017 (72): 231-244.

[5] Shukla A P, Agarwal S. An enhanced cellular automata based scheme for noise filtering [J]. International Journal of Signal Processing, Image Processing and Pattern Recognition, 2014, 7 (4): 231-242.

[6] Priego B, Duro R J, Chanussot J. Cellular automata-based image sequence denoising algorithm for signal dependent noise [C]// Proc of International Work-Conference on the Interplay Between Natural and Artificial Computation. Cham: Springer-Verlag, 2017: 333-342.

[7] Qi W, Han J, Zhang Y, et al. Infrared image enhancement using cellular automata [J]. Infrared Physics & Technology, 2016 (76): 684-690.

[8] Dakua S P, Abinahed J, Al-Ansari A. Semiautomated hybrid algorithm for estimation of three-dimensional liver surface in CT using dynamic cellular automata and level-sets [J]. Journal of Medical Imaging, 2015, 2015 (2): Article ID 024006.

[9] Seredynski F, Bouvry P, Zomaya A Y. Cellular automata computations and secret key cryptography [J]. Parallel Computing, 2004, 30 (5-6): 753-766.

[10] Desbordes P, Petitjean C, Ruan S. 3D automated lymphoma segmentation in PET images based on cellular automata [C]// Proc of the 4th Image Processing Theory, Tools and Applications. [S. l.]: IEEE Press, 2014: 1-6.

[11] Sompong C, Wongthanavasu S. Brain tumor segmentation using cellular automata-based fuzzy c-means [C]// Proc of the 13th Computer Science and Software Engineering. [S. l.]: IEEE Press, 2016: 1-6.

[12] Hamamci A, Kucuk N, Karaman K, et al. Tumor-cut: segmentation of brain tumors on contrast enhanced MR images for radiosurgery applications [J]. IEEE Trans on Medical Imaging, 2012, 31 (3): 790-804.

[13] Sachdeva J, Kumar V, Gupta I, et al. A novel content-based active contour model for brain tumor segmentation [J]. Magnetic Resonance Imaging, 2012, 30 (5): 694-715.

[14] Randhawa R S, Modi A, Jain P, et al. Improving Boundary Classification for Brain Tumor Segmentation and Longitudinal Disease Progression [C]// Proc of International Workshop on Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries. Cham: Springer-Verlag, 2016: 65-74.

[15] Cao Yiqin, Lei Zhangming, Huang Xiaosheng. Region-based algorithm for non-sampling morphological wavelet medical image fusion [J]. Application Research of Computers, 2012, 29 (6): 2379-2381.

[16] Deng A, Wu J, Yang S. An image fusion algorithm based on discrete wavelet transform and canny operator [M]// Advanced Research on Computer Education, Simulation and Modeling, Volume 175 of the Series Communications in Computer and Information Science. Berlin: Springer-Verlag, 2011: 32-38.

[17] Chao Rui, Zhang Ke, Li Yanjun. An Image Fusion Algorithm Using Wavelet Transform [J]. Acta Electronica Sinica, 2004, 32 (5): 750-753.

[18] Yu Wangyang, Chen Xiangguang, Dong Shoulong, et al. Study on image fusion algorithm based on wavelet transform [J]. Trans of Beijing Institute of Technology, 2014, 34 (12): 1262-1266.

[19] Hamamci A, Unal G, Kucuk N, et al. Cellular automata segmentation of brain tumors on post contrast MR images [C]// Proc of International Conference on Medical Image Computing and Computer-Assisted Intervention. Heidelberg: Springer-Verlag, 2010: 137-146.

[20] Bianchi A, Miller J V, Tan E T, et al. Brain tumor segmentation with symmetric texture and symmetric intensity-based decision forests [C]// Proc of the 10th International Symposium on Biomedical Imaging. San Francisco: IEEE Press, 2013: 748-751.

[21] Chaddad A, Tanougast C. Quantitative evaluation of robust skull stripping and tumor detection applied to axial MR images [J]. Brain Informatics, 2016, 3 (1): 53-61.

[22] Cordova J S, Schreibmann E, Hadjipanayis C G, et al. Quantitative tumor segmentation for evaluation of extent of glioblastoma resection to facilitate multisite clinical trials [J]. Translational Oncology, 2014, 7 (1): 40-W5.

Note: Figure translations are in progress. See original paper for figures.